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Title of the presentation

An equation based on MIR spectra to explore the genetic determinism of spontaneous lipolysis in dairy cows

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ABSTRACT

Mid infrared (MIR) spectra have been used since the late 2000s to phenotype new traits at large scale through prediction equations. It has been used in France since 2012 to quantify free fatty acids on herd milks in the framework of quality-based milk payment system. In addition to the loss of income, a high lipolysis level leads to a degradation of organoleptic (rancid taste) and technological (processing inability) properties of milk. Monitoring lipolysis is required to maintain the quality of milk and dairy products.

Lipolysis depends on many factors: genetics, farming practices, milking equipment, transformation process. Regarding genetics, Vanbergue highlighted in 2017 the existence of a genetic susceptibility to spontaneous lipolysis. The present study aims to investigate this issue further, by studying the genetic determinism of spontaneous lipolysis in a larger number of cows. This work is carried out within the framework of the LIPOMEC project which aims to better understand the molecular mechanisms controlling the degradation of milk fat.

Studying the genetic determinism of lipolysis requires the phenotyping of a large number of cows. As the equation initially developed on herd milk was not fully appropriate for individual milks (range, precision), a new prediction equation was estimated from the MIR spectra of individual milks. For this purpose, 432 milk samples were collected in 4 experimental farms in 2018 (approximately 40 cows per farm sampled 2 or 3 times a year) to maximize the variability of breeds (Holstein, Normande, Montbéliarde) and diets. A joint analysis of lipolysis according ISO/TS 22113 standard (BDI method) and by MIR spectrometry was carried out on each sample. Lipolysis measured by BDI method averaged 0.53 mmol/100 g fat (sd=0.41 mmol/100 g fat). The equation was developed by Partial Least Square regression after LOG transformation. Its coefficient of determination R^2 reached 0.72, with a residual standard deviation Sy,x of 0.19 mmol/100 g of fat. The equation was then applied to obtain phenotypes on more than 300,000 MIR milk spectra from Holstein, Normande and Montbéliarde breeds. Genetic parameters were estimated using a repeatability animal model.

Heritability and repeatability estimates were 0.21 and 0.40 in both Normande and Hostein breeds but higher (0.31 and 0.46) in Montbéliarde breed.

This work opens the opportunity to new uses of MIR spectra to improve the control of lipolysis in farm, by a closer management of the herd, or even by selection.

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